WEST

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Database: US Patents Full-Text Database

Term: ashkenazi-avi$.in.

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Search History

DB Name	Query	Hit Count	Set Name
USPT	ashkenazi-avi$.in.	4	L5
USPT	l3 and (apopt$ or tnf$)	31	L4
USPT	l1 or l2	20294	L3
USPT	LIT or TR5	20161	L2
USPT	Apo-2DcR or TRAIL-3 or TRID or DcR1	134	L1

AC W64668;
DT 23-OCT-1998 (first entry)
DE Human TRID protein.
KW TRAIL receptor without intracellular domain; TRID; TNFR-5; human;
KW tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
KW haematopoietic tissue; immune system; ligand; apoptosis; treatment.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= signal
FT Protein 27..259
FT /label= TRID
FT Region 42..52
FT /label= epitope
FT Region 58..66
FT /label= epitope
FT Region 68..76
FT /label= epitope
FT Region 79..85
FT /label= epitope
FT Region 91..102
FT /label= epitope
FT Region 110..122
FT /label= epitope
FT Region 126..136
FT /label= epitope
FT Region 142..148
FT /label= epitope
PN WO9830693-A2.
PD 16-JUL-1998.
PF 13-JAN-1998; U00152.
PR 07-AUG-1997; US-054885.
PR 14-JAN-1997; US-035496.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y,
PI Yu G;
DR WPI; 98-399141/34.
DR N-PSDB; V51348.
PT Human TRAIL receptor without an intracellular domain polypeptide -
PT used in the diagnosis of immune system-related disorder(s)
PS Claim 1b; Fig 1; 90pp; English.
CC This sequence represents a human TRID (TRAIL (TNF-related
CC apoptosis-inducing ligand) receptor without an intracellular domain).
CC TRID is a member of the tumour necrosis factor receptor (TNFR) family
CC also known as TNFR-5. TRID is expressed in haematopoietic tissues and
CC other normal human tissues. For a number of immune system-related
CC disorders, substantially altered (whether increased or decreased) levels
CC of TRID gene expression can be detected, therefore the TRID polypeptides,
CC nucleic acids and antibodies are useful in the diagnosis of such immune
CC system related disorders. Mutations of the TRID gene can also be
CC detected. TRID can also be used to identify ligands which may be useful
CC in the treatment of apoptosis related disorders. TRID is administered to
CC humans at a parenteral dose of 0.01 to 1 mg/kg/day.
SQ Sequence 259 AA;

Query Match 100.0%; Score 1783; DB 34; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.42e-127;

AC W76331;
DT 11-JAN-1999 (first entry)
DE Human tumour necrosis related receptor TR5.
KW Tumour necrosis related receptor; TR5; human; inflammation;
KW arthritis; septicaemia; transplant rejection; autoimmune disease;
KW inflammatory bowel disease; graft versus host disease; infection;
KW stroke; ischaemia; acute respiratory disease syndrome; psoriasis;
KW restenosis; brain injury; AIDS; bone disease; cancer;
KW atherosclerosis; Alzheimer's disease; therapy; diagnosis.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Peptide   1..165
FT   /label= Sig_peptide
FT Protein   66..299
FT   /label= Mat_protein
PN EP-867509-A2.
PD 30-SEP-1998.
PF 04-FEB-1998; 300827.
PR 28-JUL-1997; US-901469.
PR 05-FEB-1997; US-795910.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Lyn SDP, Tan KB, Truneh A, Young PR;
DR WPI; 98-497862/43.
DR N-PSDB; V56990.
PT New polynucleotide encoding TR5 polypeptide - used to diagnose,
PT prevent and treat e.g. inflammation, arthritis, septicaemia,
PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,
PT restenosis, brain injury, AIDS and bone diseases
PS Claim 5; Fig 1; 22pp; English.
CC This is the amino acid sequence of human tumour necrosis related
CC receptor TR5, as deduced from the sequence of an isolated cDNA
CC clone (see V56990). The protein is characterised as a GPI-linked
CC protein that has a membrane proximal O-glycosylation region. The
CC invention provides methods for the recombinant production of TR5
CC and its use in diagnostic and therapeutic methods. Treatment of a
CC subject in need of enhanced TR5 activity comprises administering an
CC agonist to the polypeptide and/or providing TR5 polynucleotide in a
CC form so as to effect production of the polypeptide activity in vivo.
CC Treatment of a subject with the need to inhibit TR5 polypeptide
CC activity comprises administering an antagonist to the polypeptide,
CC administering a nucleic acid that inhibits the expression of the
CC nucleotide sequence encoding the polypeptide and/or administering a
CC polypeptide that competes with the polypeptide for its ligand,
CC substrate or receptor. Diagnosing a disease or a susceptibility
CC to a disease related to expression or activity of TR5 polypeptide,
CC comprises determining the presence or absence of mutation in the
CC nucleotide sequence encoding the TR5 polypeptide in the genome of
CC the subject and/or analysing for the presence or amount of TR5
CC polypeptide expression in a sample. Identification of compounds
CC which bind to TR5 comprises contacting host cells with a candidate
CC compound and assessing the ability of it to bind to the cells. The
CC active agents can be used for the treatment of chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection,
CC graft vs host disease, infection, stroke, ischaemia, acute
CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone
CC diseases, cancer (e.g. lymphoproliferative disorders),

CC atherosclerosis and Alzheimer's disease.
SQ Sequence 299 AA;

Query Match 100.0%; Score 1783; DB 36; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.42e-127;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      41 maripktlkfvvvivavllpvlaysattarqeevpqqtvapqqqrhsfkgeecpagshrs 100
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Db     101 ehtgacnpctegvdytnasnnepscfpctvcksdqkhkssctmtrdtvcqckegtfrnen 160
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AC W64483;
DT 20-OCT-1998 (first entry)
DE Human DR4 protein.
KW Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease;
KW infection; graft rejection; antagonist; inhibitor; diagnostic.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Peptide   1..23
FT   /label= signal
FT Protein   24..468
FT   /label= DR4
FT Domain   24..238
FT   /label= extracellular_domain
FT Domain   239..264
FT   /label= transmembrane_domain
FT Domain   265..468
FT   /label= intracellular domain
FT Domain   379..422
FT   /label= death_domain
PN WO9832856-A1.
PD 30-JUL-1998.
PF 27-JAN-1998; U01464.
PR 05-FEB-1997; US-037829.
PR 28-JAN-1997; US-035722.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PI Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;
DR WPI; 98-427952/36.
DR N-PSDB; V49527.
PT Nucleic acid encoding human death domain-containing receptor 4 -
PT useful for therapeutic modulation of apoptosis, in e.g. cancer and
PT autoimmune diseases
PS Claim 1a; Fig 1; 92pp; English.
CC This sequence represents a human death domain containing receptor 4, DR4.
CC DR4 agonists are used to increase apoptosis induced by tumour necrosis
CC factor (TNF)-family ligands, e.g. in cases of cancer, autoimmune disease,
CC viral or other infections, inflammation, graft vs. host disease, acute or
CC chronic graft rejection. Antagonists of DR4 are used to inhibit such
CC apoptosis, e.g. in cases of acquired immune deficiency syndrome,
CC neurodegenerative disease, myelodysplastic syndrome, ischaemic injury,
CC toxin-induced liver damage, septic shock, cachexia and anorexia, also a
CC wide range of inflammatory conditions. DR4 of fragments of the protein
CC are used diagnostically, e.g. to detect mutant forms of DR4 (possibly
CC associated with disease), for isolating the DR4 gene or related sequences
CC and for chromosomal mapping.
SQ Sequence 468 AA;

Query Match 34.6%; Score 617; DB 34; Length 468;
Best Local Similarity 60.4%; Pred. No. 8.48e-37;
Matches 90; Conservative 24; Mismatches 29; Indels 6; Gaps 3;

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Db     87 rvhktfkfvvv--gvllqvvpssaatiklhd---qsigtqqwehsplgelcppgshrser 141
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Qy      3 RIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH 62

Db    142 pgacnrctegvgytnasnnlfaclpctacksdeeerspctttrntacqckpgtfrndnsa 201
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Apo-2DcR SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1783	100.0	259	15	US-09-006-	Sequence 2, Applicatio	1.98e-136
2	1783	100.0	259	14	US-08-924-	Sequence 6, Applicatio	1.98e-136
3	1783	100.0	259	2	US-60-035-	Sequence 2, Applicatio	1.98e-136
4	1783	100.0	259	13	US-08-878-	Sequence 1, Applicatio	1.98e-136
5	1783	100.0	259	15	US-09-096-	Sequence 1, Applicatio	1.98e-136
6	1783	100.0	259	13	US-08-878-	Sequence 1, Applicatio	1.98e-136
7	1783	100.0	299	17	US-09-205-	Sequence 11, Applicati	1.98e-136
8	1783	100.0	299	12	US-08-795-	Sequence 2, Applicatio	1.98e-136
9	1783	100.0	299	13	US-08-878-	Sequence 3, Applicatio	1.98e-136
10	1783	100.0	299	15	US-09-096-	Sequence 3, Applicatio	1.98e-136
11	1783	100.0	299	1	PCT-US98-1	Sequence 2, Applicatio	1.98e-136
12	1783	100.0	299	17	US-09-266-	Sequence 8, Applicatio	1.98e-136
13	1783	100.0	299	16	US-09-134-	Sequence 4, Applicatio	1.98e-136
14	1783	100.0	299	13	US-08-883-	Sequence 2, Applicatio	1.98e-136
15	1783	100.0	299	17	US-09-229-	Sequence 2, Applicatio	1.98e-136
16	1783	100.0	299	15	US-09-079-	Sequence 2, Applicatio	1.98e-136
17	1783	100.0	299	1	PCT-US99-0	Sequence 8, Applicatio	1.98e-136
18	1783	100.0	299	13	US-08-878-	Sequence 3, Applicatio	1.98e-136
19	1783	100.0	299	14	US-08-901-	Sequence 2, Applicatio	1.98e-136
20	823	46.2	386	16	US-09-130-	Sequence 6, Applicatio	7.60e-56
21	823	46.2	386	13	US-08-892-	Sequence 2, Applicatio	7.60e-56

AC O14798;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CYTOTOXIC TRAIL RECEPTOR-3.
GN TRAIL-R3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,
RA COHEN G.M., ALNEMRI E.S.;
RL J. BIOL. CHEM. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97461602.
RA DEGLI-ESPOSTI M.A., SMOLAK P.J., WALCZAK H., WAUGH J., HUANG C.P.,
RA DUBOSE R.F., GOODWIN R.G., SMITH C.A.;
RT "Cloning and characterization of TRAIL-R3, a novel member of the
RT emerging TRAIL receptor family.";
RL J. EXP. MED. 186:1165-1170(1997).
DR EMBL; AF020502; G2443820; -.
DR EMBL; AF014794; G2957264; -.
DR PFAM; PF00020; TNFR_c6; 2.
SQ SEQUENCE   299 AA; 31759 MW; 59B93A14 CRC32;

Query Match 100.0%; Score 1783; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.82e-237;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRS 60

Db    101 EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN 160
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Db    161 SPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAE 220
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Qy    181 ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240

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Qy    241 LSCTIVGIIVLIVLLIVFV 259
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AC   O14755;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   TRAIL RECEPTOR 3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC   CATARRHINI; HOMINIDAE; HOMO.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER, AND SPLEEN;
RA   SCHNEIDER P., BODMER J.-L., THOME M., HOLLER N., HOFMANN K.,
RA   TSCHOPP J.;
RL   FEBS LETT. 0:0-0(1997).
DR   EMBL; AF016267; G2529565; -.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   259 AA;  27365 MW;  3C196935 CRC32;
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Db       1 MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRS 60
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Db      61 EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNVN 120
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Db     121 SPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAE 180
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Db     181 ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240
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Qy     241 LSCTIVGIIVLIVLLIVFV 259
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LOCUS AF012536 1180 bp mRNA PRI 21-AUG-1997
DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.
ACCESSION AF012536
NID g2338421
VERSION AF012536.1 GI:2338421
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1180)
AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M.,
Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I.,
Goddard,A.D., Godowski,P. and Ashkenazi,A.
TITLE Control of TRAIL-induced apoptosis by a family of signaling and
decoy receptors
JOURNAL Science 277 (5327), 818-821 (1997)
MEDLINE 97390509
REFERENCE 2 (bases 1 to 1180)
AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D.,
Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D.,
Godowski,P. and Ashkenazi,A.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
source 1. .1180
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gene 1. .1180
/gene="DcR1"
CDS 193. .972
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inhibits apoptosis induction by TRAIL/Apo2L"
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BASE COUNT 338 a 326 c 298 g 218 t
ORIGIN

Query Match 100.0%; Score 1180; DB 11; Length 1180;
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Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS       AF033854     1377 bp    mRNA            PRI       27-NOV-1997
DEFINITION  Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete
            cds.
ACCESSION   AF033854
NID         g2645841
VERSION     AF033854.1  GI:2645841
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,
            Bell,J.I. and Screaton,G.R.
  TITLE     Lymphocyte inhibitor of TRAIL: A new receptor protecting
            lymphocytes from the death ligand TRAIL
  JOURNAL   J. Immunol. (1997) In press
REFERENCE   2  (bases 1 to 1377)
  AUTHORS   Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,
            Bell,J.I. and Screaton,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-1997) Immunology, Institute of Molecular
            Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK
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ORIGIN
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Qy      17 CACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAGAGATGC 76
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Db       1 CACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAGAGATGC 60
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Qy      77 AAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGGCCGC 136
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Qy     137 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACCATGG 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACCATGG 180

Qy     197 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCAGTCC 256
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Db     181 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCAGTCC 240

Qy     257 TAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 316
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Db     241 TAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 300

Qy     317 AGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376
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Qy     377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 436
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Db     361 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 420

Qy     437 AACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCA 496
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Db     421 AACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCA 480

Qy     497 CCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACTCCC 556
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Qy     617 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCC 676
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Qy     677 CAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGA 736
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Qy     737 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 796
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Db     721 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 780

Qy     797 CGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCC 856
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Db     781 CGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCC 840

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LOCUS AF016267 1388 bp mRNA PRI 04-MAR-1999
DEFINITION Homo sapiens TRAIL receptor 3 mRNA, complete cds.
ACCESSION AF016267
NID g2529564
VERSION AF016267.1 GI:2529564
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1388)
AUTHORS Schneider,P., Bodmer,J.L., Thome,M., Hofmann,K., Holler,N. and
Tschopp,J.
TITLE Characterization of two receptors for TRAIL
JOURNAL FEBS Lett. 416 (3), 329-334 (1997)
MEDLINE 98039016
REFERENCE 2 (bases 1 to 1388)
AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and
Tschopp,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) Institute of Biochemistry, University of
Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066,
Switzerland
FEATURES Location/Qualifiers
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BASE COUNT 331 a 415 c 368 g 274 t
ORIGIN

Query Match 91.7%; Score 1081.8; DB 42; Length 1388;
Best Local Similarity 99.7%; Pred. No. 2e-215;
Matches 1094; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      77 AAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGGCCGC 136
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Qy    137 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACCATGG 196
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Db    552 CAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTA 611

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Qy    677 CAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGA 736
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Db    672 CAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGA 731

Qy    737 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 796
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Db    732 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 791

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Db    792 CGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCC 851

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Qy     977 CTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGTAGGCGCTGGCTGAGGG 1036
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Qy    1037 CGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAAC 1096
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Db    1032 CGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAAC 1091

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Db    1092 GCCTGCCCCTGCCCCAA 1108
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LOCUS AF014794 1365 bp mRNA PRI 13-MAR-1998
DEFINITION Homo sapiens TNF related TRAIL receptor (TRAIL-R3) mRNA, complete cds.
ACCESSION AF014794
NID g2957263
VERSION AF014794.1 GI:2957263
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1365)
AUTHORS Degli-Esposti,M.A., Smolak,P.J., Walczak,H., Waugh,J., Huang,C.P., DuBose,R.F., Goodwin,R.G. and Smith,C.A.
TITLE Cloning and characterization of TRAIL-R3, a novel member of the emerging TRAIL receptor family
JOURNAL J. Exp. Med. 186 (7), 1165-1170 (1997)
MEDLINE 97461602
REFERENCE 2 (bases 1 to 1365)
AUTHORS Degli-Esposti,M.A.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1997) Biochemistry, Immunex, 51 University Street, Seattle, WA 98101, USA
FEATURES Location/Qualifiers
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CDS 30. .929
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BASE COUNT 332 a 403 c 363 g 267 t
ORIGIN

Query Match 89.6%; Score 1057; DB 11; Length 1365;
Best Local Similarity 100.0%; Pred. No. 2.8e-210;
Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      14 GGGAGTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGG 73

Qy     117 GGACAGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGG 176
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Db       74 GGACAGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGG 133

Qy      177 CGTCGGGAACCATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGT 236
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Qy      357 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTA 416
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LOCUS AF020502 900 bp mRNA PRI 04-MAR-1999
DEFINITION Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete cds.
ACCESSION AF020502
VERSION AF020502.1 GI:2443819
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T., Cohen,G.M. and Alnemri,E.S.
TITLE Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL
JOURNAL J. Biol. Chem. 272 (41), 25417-25420 (1997)
MEDLINE 97467318
REFERENCE 2 (bases 1 to 900)
AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T., Cohen,G.M. and Alnemri,E.S.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology, Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA 19107, USA
FEATURES Location/Qualifiers
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gene 1. .900
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CDS 1. .900
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BASE COUNT 228 a 262 c 240 g 170 t
ORIGIN

Query Match 76.1%; Score 898.4; DB 42; Length 900;
Best Local Similarity 99.9%; Pred. No. 2.3e-177;
Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGG 132
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Db    541 TGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAA 600

Qy    673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 732
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Db    601 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 660

Qy    733 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 792
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Db    661 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 720

Qy    793 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 852
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Db    721 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 780

Qy    853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 912
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Db    781 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 840

Qy    913 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 972
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Db    841 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 900
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LOCUS AF012629 780 bp mRNA PRI 21-AUG-1997
DEFINITION Homo sapiens antagonist decoy receptor for TRAIL/Apo-2L (TRID) mRNA, complete cds.
ACCESSION AF012629
NID g2338430
VERSION AF012629.1 GI:2338430
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 780)
AUTHORS Pan,G., Ni,J., Wei,Y.F., Yu,G., Gentz,R. and Dixit,V.M.
TITLE An antagonist decoy receptor and a death domain-containing receptor for TRAIL
JOURNAL Science 277 (5327), 815-818 (1997)
MEDLINE 97390508
REFERENCE 2 (bases 1 to 780)
AUTHORS Pan,G., Ni,J., Wei,Y., Yu,G., Gentz,R. and Dixit,V.M.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1997) Pathology, University of Michigan, 1301 Catherine Road, Room 7518, Ann Arbor, MI 48109, USA
FEATURES Location/Qualifiers
source 1. .780
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .780
/gene="TRID"
CDS 1. .780
/gene="TRID"
/codon_start=1
/product="antagonist decoy receptor for TRAIL/Apo-2L"
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/translation="MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQ
RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCT
MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVE
TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPG
TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"
BASE COUNT 202 a 226 c 196 g 156 t
ORIGIN

Query Match 66.1%; Score 780; DB 11; Length 780;
Best Local Similarity 100.0%; Pred. No. 8.9e-153;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     193 ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA 252
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Db       1 ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA 60

Qy     253 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCC 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCC 120

Qy     313 CCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372
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Db     121 CCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 180

Qy     373 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432

Db     181 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 240

Qy     433 AATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCC 492

Db     241 AATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCC 300

Qy     493 TGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAAC 552

Db     301 TGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAAC 360

Qy     553 TCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAAT 612

Db     361 TCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAAT 420

Qy     613 TGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAA 672

Db     421 TGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAA 480

Qy     673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 732

Db     481 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 540

Qy     733 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 792

Db     541 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 600

Qy     793 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 852

Db     601 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 660

Qy     853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 912

Db     661 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 720

Qy     913 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 972

Db     721 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 780
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LOCUS       AF029761     1726 bp    mRNA             PRI       08-JAN-1999
DEFINITION  Homo sapiens decoy receptor 2 mRNA, complete cds.
ACCESSION   AF029761
NID         g4106963
VERSION     AF029761.1  GI:4106963
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1726)
  AUTHORS   Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,
            Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and
            Ashkenazi,A.
  TITLE     A novel receptor for Apo2L/TRAIL contains a truncated death domain
  JOURNAL   Curr. Biol. 7 (12), 1003-1006 (1997)
  MEDLINE   98044290
REFERENCE   2  (bases 1 to 1726)
  AUTHORS   Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,
            Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and
            Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1997) Molecular Oncology, Genentech, 1 DNA Way,
            South San Francisco, CA 94080, USA
REFERENCE   3  (bases 1 to 1726)
  AUTHORS   Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,
            Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and
            Ashkenazi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-1999) Molecular Oncology, Genentech, 1 DNA Way,
            South San Francisco, CA 94080, USA
  REMARK    Sequence update by submitter
COMMENT     On Jan 6, 1999 this sequence version replaced gi:2688980.
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     source          1. .1726
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                     /map="8p21"
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                     contains a truncated death domain"
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                     /product="decoy receptor 2"
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                     /db_xref="PID:g2688981"
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                     VAVLLPVRVDSATIPRQDEVPQQTVAPQQQRRSLKEEECPAGSHRSEYTGACNPCTEG
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                     GCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVV
                     LVIILAVVVVGFSCRKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNAR
                     NETLSNRYLQPTQVSEQEIQGQELAELTGVTVESPEEPQRLLEQAEAEGCQRRRLLVP
                     VNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYEEDEAGSATSCL"
BASE COUNT      440 a    432 c    443 g    411 t
ORIGIN
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Query Match 36.5%; Score 430.2; DB 11; Length 1726;
Best Local Similarity 77.7%; Pred. No. 3.8e-80;
Matches 579; Conservative 0; Mismatches 143; Indels 23; Gaps 4;

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Qy       6 GGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTG 65
           | |||||| | |||||||||| ||||  |   |||||||||||| |||||||||   |||
Db       2 GAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTTGGCGCTTTC 61

Qy      66 ACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGC 125
                           ||    | |      |      | | || ||| |||||||| |||
Db      62 ------------------GATCCACCCTCCTCCCTTCTCATGGGACTTTGGGGACAAAGC 103

Qy     126 GCCCCGGCCGCCT-GATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGA 184
           | |||| |||||| ||  ||    |||||| || | |||||| ||||||| |||||||||
Db     104 GTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCAGGACAGCGTCGGGA 163
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AC V84347;
DT 26-APR-1999 (first entry)
DE Human Apo-2DcR cDNA clone DNA33085.
KW Apo-2DcR; human; apoptosis; tumour necrosis factor receptor;
KW neurodegeneration; autoimmune disease; inflammation; cancer;
KW therapy; ds.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT CDS   193. .972
FT   /*tag= a
FT sig_peptide   193. .279
FT   /*tag= b
FT mat_peptide   280. .969
FT   /*tag= c
FT CDS   93. .972
FT   /*tag= d
FT   /note= "alternative translational initiation
FT   site at 93. .95, encodes amino acid
FT   residues -40 to 259 of Apo-2DcR"
PN WO9858062-A1.
PD 23-DEC-1998.
PF 12-JUN-1998; U12456.
PR 18-JUN-1997; US-878168.
PA (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A,
PI Kim KJ, Wood WI;
DR WPI; 99-095340/08.
DR P-PSDB; W84347.
PT New Apo-2DcR polypeptide - used for modulation and diagnosis of
PT apoptosis, e.g. in neurodegeneration
PS Claim 36; Page 51-53; 88pp; English.
CC cDNA clone DNA33085 codes for human Apo-2DcR (see W88408), a novel
CC member of the tumour necrosis factor receptor family that binds to
CC Apo-2 ligand. It was isolated by: transformation of yeast with a
CC vector incorporating human breast carcinoma cDNA; isolation of
CC yeast clones secreting amylase; PCR amplification (see V84349-50)
CC of the insert directly from the yeast colony and purification of
CC DNA for sequencing; use of an isolated sequence (DNA21705) as a
CC probe to screen a human foetal lung library; and isolation of the
CC full-length clone, which is deposited as ATCC 209087. An
CC alternative translational initiation site encodes amino acid
CC residues -40 to 259 of Apo-2DcR (see W88409). The invention
CC provides vectors and host cells for recombinant production of
CC Apo-2DcR polypeptides, antibodies, and transgenic and knockout
CC animals (useful e.g. for screening and developing drugs that protect
CC against excessive apoptosis). Apo-2DcR, or chimeras comprising
CC Apo-2DcR or its extracellular domain fused to a heterologous
CC polypeptide are used to modulate apoptosis of mammalian cells
CC (claimed) and/or NF-kappaB activation by Apo-2 ligand, and may be
CC expressed in vivo or ex vivo for gene therapy. They can be used in
CC methods for the modulation and diagnosis of apoptosis e.g. in cases
CC of neurodegeneration, autoimmune diseases and inflammation. Most
CC human tumour cells do not express Apo-2DcR transcripts, but normal
CC tissues do, suggesting that Apo-2DcR may permit selective killing
CC of cancer cells by Apo-2 ligand, possibly by protecting normal, but
CC not cancerous, cells.
SQ Sequence 1180 BP; 338 A; 326 C; 298 G; 218 T;

Query Match 100.0%; Score 1180; DB 1; Length 1180;
Best Local Similarity 100.0%; Pred. No. 5.8e-240;
Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGA 60
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Db       1 GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGA 60

Qy      61 GTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGAC 120

Qy     121 AGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTC 180
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Db     121 AGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTC 180

Qy     181 GGGAACCATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCG 240
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Db     181 GGGAACCATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCG 240

Qy     241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAG 300
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Db     241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAG 300

Qy     301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGA 360
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Db     301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGA 360

Qy     361 TCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACC 420
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Qy     421 AACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAA 480
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Db     421 AACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAA 480

Qy     481 CATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTC 540
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Db     481 CATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTC 540

Qy     541 CGGAATGAAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTC 600
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Db     541 CGGAATGAAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTC 600

Qy     601 CAAGTCAGTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAAT 660
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Db     601 CAAGTCAGTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAAT 660

Qy     661 GCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCC 720
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Db     661 GCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCC 720

Qy     721 CCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAG 780
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Db     721 CCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAG 780
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Qy     781 ACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGC 840
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Db     781 ACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGC 840

Qy     841 CCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCC 900
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Db     841 CCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCC 900

Qy     901 TCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATT 960
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Db     901 TCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATT 960

Qy     961 GTGTTTGTTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGT 1020
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Db     961 GTGTTTGTTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGT 1020

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Qy    1081 TCCCACAGACAGAAACGCCTGCCCCTGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1140
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Db    1081 TCCCACAGACAGAAACGCCTGCCCCTGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1140

Qy    1141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1180
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Db    1141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1180
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RESULT   2
V56990
ID   V56990 standard; cDNA; 1410 BP.
AC   V56990;
DT   11-JAN-1999  (first entry)
DE   Human tumour necrosis related receptor TR5 cDNA.
KW   Tumour necrosis related receptor; TR5; human; inflammation;
KW   arthritis; septicaemia; transplant rejection; autoimmune disease;
KW   inflammatory bowel disease; graft versus host disease; infection;
KW   stroke; ischaemia; acute respiratory disease syndrome; psoriasis;
KW   restenosis; brain injury; AIDS; bone disease; cancer;
KW   atherosclerosis; Alzheimer's disease; therapy; diagnosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             69. .968
FT                   /*tag=  a
FT   sig_peptide     69. .263
FT                   /*tag=  b
FT   mat_peptide     264. .965
FT                   /*tag=  b
PN   EP-867509-A2.
PD   30-SEP-1998.
PF   04-FEB-1998; 300827.
PR   28-JUL-1997; US-901469.
PR   05-FEB-1997; US-795910.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PI   Lyn SDP, Tan KB, Truneh A, Young PR;
```

DR WPI; 98-497862/43.
DR P-PSDB; W76331.
PT New polynucleotide encoding TR5 polypeptide - used to diagnose,
PT prevent and treat e.g. inflammation, arthritis, septicaemia,
PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,
PT restenosis, brain injury, AIDS and bone diseases
PS Claim 4; Fig 1; 22pp; English.
CC This nucleotide sequence codes for human tumour necrosis related
CC receptor, TR5 (see W76331). An expressed sequence tag (EST 213397)
CC derived from a cDNA libray made from human prostate was found to
CC have sequence similarity to the human tumour necrosis factor (TNF)
CC receptor. A search through several overlapping ESTs indicated that
CC this represented the 5' most EST of the assemble and so it was
CC completely sequenced. Analysis of the 1410 cDNA sequence indicated
CC that it encoded a complete open reading frame for a novel member of
CC the TNF receptor superfamily. A polynucleotide encoding TR5 can
CC be obtained from a cDNA library derived from mRNA in cells of
CC prostate, endothelial cells, interleukin-1 beta-treated smooth
CC muscle cells, foetal liver spleen cells, and pregnant uterus using
CC expressed sequence tag analysis. Treatment of a subject in need of
CC enhanced TR5 polypeptide activity comprises administering an agonist
CC to the polypeptide and/or providing TR5 polynucleotide in a form so
CC as to effect production of the polypeptide activity in vivo.
CC Treatment of a subject with the need to inhibit TR5 polypeptide
CC activity comprises administering an antagonist to the polypeptide,
CC administering a nucleic acid that inhibits the expression of the
CC nucleotide sequence encoding the polypeptide and/or administering a
CC polypeptide that competes with the polypeptide for its ligand,
CC substrate or receptor. Diagnosing a disease or a susceptibility
CC to a disease related to expression or activity of TR5 polypeptide,
CC comprises determining the presence or absence of mutation in the
CC nucleotide sequence encoding the TR5 polypeptide in the genome of
CC the subject and/or analysing for the presence or amount of TR5
CC polypeptide expression in a sample. Identification of compounds
CC which bind to TR5 comprises contacting host cells with a candidate
CC compound and assessing the ability of it to bind to the cells. The
CC active agents can be used for the treatment of chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection,
CC graft vs host disease, infection, stroke, ischaemia, acute
CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone
CC diseases, cancer (e.g. lymphoproliferative disorders),
CC atherosclerosis and Alzheimer's disease.
SQ Sequence 1410 BP; 342 A; 420 C; 371 G; 277 T;

Query Match 93.6%; Score 1104.4; DB 1; Length 1410;
Best Local Similarity 99.9%; Pred. No. 4.9e-224;
Matches 1105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      8 GAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGAC 67
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Qy     68 CAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGC 127
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Db     64 CAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGC 123
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Qy     128 CCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACC 187
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Db     124 CCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACC 183

Qy     188 ATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGC 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 ATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGC 243

Qy     248 TGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAG 307
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 TGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAG 303

Qy     308 TGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATA 367
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 TGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATA 363

Qy     368 GATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTT 427
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 GATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTT 423

Qy     428 CCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAA 487
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 CCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAA 483

Qy     488 GTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATG 547
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 GTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATG 543

Qy     548 AAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCA 607
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 AAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCA 603

Qy     608 GTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTG 667
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 GTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTG 663

Qy     668 TGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTG 727
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 TGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTG 723

Qy     728 CTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGA 787
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 CTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGA 783

Qy     788 CCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGA 847
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 CCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGA 843

Qy     848 CTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTC 907
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 CTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTC 903

Qy     908 ATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTG 967
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 ATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTG 963
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Qy     968 TTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGTAGGCGCT 1027
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     964 TTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGTAGGCGCT 1023

Qy    1028 GGCTGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACA 1087
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1024 GGCTGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACA 1083

Qy    1088 GACAGAAACGCCTGCCCCTGCCCCAA 1113
           |||||||||||||||||||||||||||
Db    1084 GACAGAAACGCCTGCCCCTGCCCCAA 1109


RESULT   3
V51348
ID   V51348 standard; DNA; 1392 BP.
AC   V51348;
DT   23-OCT-1998  (first entry)
DE   Human TRID genomic DNA.
KW   TRAIL receptor without intracellular domain; TRID; TNFR-5; human;
KW   tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
KW   haematopoietic tissue; immune system; ligand; apoptosis; treatment; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             183. .962
FT                   /*tag=  a
FT   sig_peptide     183. .260
FT                   /*tag=  b
FT   mat_peptide     261. .959
FT                   /*tag=  c
FT                   /product= "TRID"
FT                   /note= "TRAIL receptor without intracellular domain"
PN   WO9830693-A2.
PD   16-JUL-1998.
PF   13-JAN-1998; U00152.
PR   07-AUG-1997; US-054885.
PR   14-JAN-1997; US-035496.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y,
PI   Yu G;
DR   WPI; 98-399141/34.
DR   P-PSDB; W64668.
PT   Human TRAIL receptor without an intracellular domain polypeptide -
PT   used in the diagnosis of immune system-related disorder(s)
PS   Claim 2; Fig 1; 90pp; English.
CC   This sequence encodes a human TRID (TRAIL (TNF-related apoptosis-inducing
CC   ligand) receptor without an intracellular domain). TRID is a member of
CC   the tumour necrosis factor receptor (TNFR) family also known as TNFR-5.
CC   TRID is expressed in haematopoietic tissues and other normal human
CC   tissues. For a number of immune system-related disorders, substantially
CC   altered (whether increased or decreased) levels of TRID gene expression
CC   can be detected, therefore the TRID polypeptides, nucleic acids and
CC   antibodies are useful in the diagnosis of such immune system related
CC   disorders. Mutations of the TRID gene can also be detected. TRID can also
CC   be used to identify ligands which may be useful in the treatment of
CC   apoptosis related disorders. TRID is administered to humans at a
CC   parenteral dose of 0.01 to 1 mg/kg/day.
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SQ Sequence 1392 BP; 329 A; 418 C; 368 G; 277 T;

Query Match 93.5%; Score 1103; DB 1; Length 1392;
Best Local Similarity 100.0%; Pred. No. 9.7e-224;
Matches 1103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 CCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAG 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAG 60

Qy      71 AGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCC 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCC 120

Qy     131 GGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATA 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATA 180

Qy     191 CCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGC 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGC 240

Qy     251 CAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGG 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGG 300

Qy     311 CCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGAT 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGAT 360

Qy     371 CAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCA 430
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCA 420

Qy     431 ACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTT 490
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTT 480

Qy     491 CCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAA 550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAA 540

Qy     551 ACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTA 610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTA 600

Qy     611 ATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGG 670
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGG 660

Qy     671 AAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTG 730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTG 720

Qy     731 AAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCA 790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     721 AAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCA 780

Qy     791 CCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTC 850
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTC 840

Qy     851 CTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATT 910
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATT 900

Qy     911 ACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTT 970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTT 960

Qy     971 GAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGTAGGCGCTGGC 1030
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCAGGTAGGCGCTGGC 1020

Qy    1031 TGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGAC 1090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGAC 1080

Qy    1091 AGAAACGCCTGCCCCTGCCCCAA 1113
           |||||||||||||||||||||||
Db    1081 AGAAACGCCTGCCCCTGCCCCAA 1103


RESULT   4
X23412
ID   X23412 standard; DNA; 1365 BP.
AC   X23412;
DT   18-JUN-1999  (first entry)
DE   Human hAPO9 DNA.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; human; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             123. .955
FT                   /*tag=  a
FT                   /product= "APO9"
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   P-PSDB; W93578.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Example III; Fig 6; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
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CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 1365 BP; 321 A; 411 C; 362 G; 271 T;

Query Match 90.5%; Score 1067.6; DB 1; Length 1365;
Best Local Similarity 99.5%; Pred. No. 2.7e-216;
Matches 1092; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Qy      17 CACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAGAGATGC 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAGAGATGC 60

Qy      77 AAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGGCCGC 136
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      61 AAGGGGTGAAGGAGCGCTTCCTACCGTTA-GGAACTCTGGGGACAGAGCGCCCCGGCCGC 119

Qy     137 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACCATGG 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACCATGG 179

Qy     197 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCAGTCC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCAGTCC 239

Qy     257 TAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 TAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 299

Qy     317 AGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 AGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 359

Qy     377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 419

Qy     437 AACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCA 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 AACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCA 479
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Qy     497 CCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACTCCC 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACTCCC 539

Qy     557 CAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTA 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 CAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTA 599

Qy     617 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCC 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCC 659

Qy     677 CAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGA 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 CAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGA 719

Qy     737 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 CAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCC 779

Qy     797 CGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCC 856
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     780 CGGGGACTCCTGCCCCAGCTGCTGAAGAGAGAATGACCACCAGCCCGGGGACTCCTGCCC 839

Qy     857 CAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTACCTCT 916
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 CAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTACCTCT 899

Qy     917 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGAAAGA 976
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGAAAGA 959

Qy     977 CTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCA-GGTAGGCGCTGGCTGAGG 1035
           |||||||||||||||||||||||||||||||||||||||| | || |||||||||||| |
Db     960 CTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTCACGTTACGCGCTGGCTGAAG 1019

Qy    1036 GCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAA 1095
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 GCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAA 1079

Qy    1096 CGCCTGCCCCTGCCCCAA 1113
           ||||||||||||||||||
Db    1080 CGCCTGCCCCTGCCCCAA 1097
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RESULT 5
X16692
ID X16692 standard; cDNA; 1347 BP.
AC X16692;
DT 04-MAY-1999 (first entry)
DE Human TNF-related apoptosis-inducing ligand binding protein cDNA.
KW Human; TNF-related apoptosis-inducing ligand binding protein; clotting;
KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;
KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;
KW haemolytic-uraemic syndrome; systemic lupus erythematosus; ss.
OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 24. .923
FT /*tag= a
PN WO9900423-A1.
PD 07-JAN-1999.
PF 25-JUN-1998; U13491.
PR 26-JUN-1997; US-883529.
PA (IMMV) IMMUNEX CORP.
PI Smith CA, Walczak H;
DR WPI; 99-095685/08.
DR P-PSDB; W94671.
PT New isolated TRAIL binding protein - which binds to a tumour
PT necrosis factor-related apoptosis inducing ligand, used in the
PT diagnosis and treatment of TRAIL-mediated disorders
PS Claim 1; Fig 1; 47pp; English.
CC The present sequence encodes human tumour necrosis factor (TNF)-related
CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be
CC used for inhibiting the biological activities of TRAIL or for purifying
CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated
CC disorder such as T cell death in HIV-infected patients. They can be used
CC for treating thrombotic microangiopathies such as thrombotic
CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small
CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic
CC acids can also be used for gene therapy. They can also be used as
CC carriers for delivering attached agents to cells bearing TRAIL.
SQ Sequence 1347 BP; 326 A; 401 C; 361 G; 259 T;

Query Match 89.6%; Score 1057; DB 1; Length 1347;
Best Local Similarity 100.0%; Pred. No. 4.6e-214;
Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      57 GGGAGTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGG 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8 GGGAGTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGG 67

Qy     117 GGACAGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGG 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 GGACAGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGG 127

Qy     177 CGTCGGGAACCATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGT 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 CGTCGGGAACCATACCATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGT 187

Qy     237 CGCGGTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCC 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 CGCGGTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCC 247

Qy     297 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGC 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     248 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGC 307

Qy     357 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTA 416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTA 367

Qy     417 CACCAACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCA 476
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      368 CACCAACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCA 427

Qy      477 AAAACATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCAC 536
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      428 AAAACATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCAC 487

Qy      537 CTTCCGGAATGAAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGA 596
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      488 CTTCCGGAATGAAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGA 547

Qy      597 AGTCCAAGTCAGTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGC 656
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      548 AGTCCAAGTCAGTAATTGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGC 607

Qy      657 CAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCC 716
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      608 CAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCC 667

Qy      717 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGA 776
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      668 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGA 727

Qy      777 AGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCAC 836
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      728 AGAGACAATGACCACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCAC 787

Qy      837 CAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCC 896
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      788 CAGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCC 847

Qy      897 TGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 956
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      848 TGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 907

Qy      957 GATTGTGTTTGTTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTC 1016
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      908 GATTGTGTTTGTTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTGAAAGGTTC 967

Qy     1017 AGGTAGGCGCTGGCTGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCT 1076
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      968 AGGTAGGCGCTGGCTGAGGGCGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCT 1027

Qy     1077 GTGTTCCCACAGACAGAAACGCCTGCCCCTGCCCCAA 1113
                ||||||||||||||||||||||||||||||||||||
Db     1028 GTGTTCCCACAGACAGAAACGCCTGCCCCTGCCCCAA 1064
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RESULT 6
X27280
ID X27280 standard; DNA; 900 BP.
AC X27280;
DT 02-JUN-1999 (first entry)
DE Human TRAIL-R3 coding sequence.
KW Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; therapy;
KW autoimmune disease; viral infection; degenerative disorder;
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;

KW cerebellar degeneration; myelodysplastic syndrome; ss.
OS Homo sapiens.
PN WO9909165-A1.
PD 25-FEB-1999.
PF 14-AUG-1998; U16945.
PR 15-AUG-1997; US-055906.
PA (IDUN-) IDUN PHARM INC.
PI Alnemri ES;
DR WPI; 99-181035/15.
DR P-PSDB; Y00933.
PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor
PT protein - useful in for screening for (ant)agonists that modulate
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
PS Claim 7; Page 62-63; 71pp; English.
CC This sequence encodes the human TRAIL receptor TRAIL-R3 of the invention.
CC An antibody against the TRAIL receptors is useful for detecting mammalian
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.
CC (Ant)agonists identified by the assay are useful for modulating the
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis
CC related conditions which are treated in this way, include cancer
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus
CC erythematosus and immune-mediated glomerulonephritis), viral infections
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic
CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial
CC infarction and stroke). The polynucleotides can also be used to treat
CC these diseases. Antisense oligonucleotides to the DNA sequences can be
CC used to form a composition that is useful for inhibiting expression of a
CC human DR5 or TRAIL-R3 protein.
SQ Sequence 900 BP; 228 A; 262 C; 240 G; 170 T;

Query Match 76.1%; Score 898.4; DB 1; Length 900;
Best Local Similarity 99.9%; Pred. No. 1e-180;
Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      73 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGG 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCGG 60

Qy     133 CCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATACC 192
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      61 CCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAAGACGGCGTCGGGAACCATACC 120

Qy     193 ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA 180

Qy     253 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCC 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCC 240

Qy     313 CCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 300
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Qy     373 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 360

Qy     433 AATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCC 420

Qy     493 TGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAAC 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAAC 480

Qy     553 TCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAAT 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAAT 540

Qy     613 TGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAA 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGTACGTCCTGGGATGATATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAA 600

Qy     673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCGGGGACTCCTGCCCCAGCTGCTGAA 660

Qy     733 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC 720

Qy     793 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCT 780

Qy     853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC 840

Qy     913 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTTGTTTGA 900
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RESULT   7
X19957
ID   X19957 standard; cDNA; 3569 BP.
AC   X19957;
DT   15-JUN-1999  (first entry)
DE   Human Tango-74 encoding cDNA.
KW   Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
KW   detection; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             104. .1264
FT                   /*tag=  a
PN   WO9907850-A1.
PD   18-FEB-1999.
PF   06-AUG-1998; U16502.
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PR 05-SEP-1997; US-058108.
PR 06-AUG-1997; US-054966.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
PI Goodearl ADJ, Holtzman DA;
DR WPI; 99-167426/14.
DR P-PSDB; Y04144.
PT New TANGO polypeptides and nucleic acids encoding them - useful as
PT diagnostic agents and for treating disorders caused by aberrant
PT expression of TANGO
PS Claim 1; Fig 3; 84pp; English.
CC The present sequence encodes human Tango-74. Tango polypeptides are
CC useful for identifying compounds which bind the polypeptide via direct
CC binding, competition binding assays or Tango-71, -73, -74, 76 or -83-
CC mediated signal transduction. Tango polypeptides are also useful for
CC identifying modulating compounds by determining effect on Tango activity.
CC Tango polypeptides and nucleic acids are useful for diagnosing diseases
CC related to aberrant expression of Tango, and Tango polypeptides are
CC useful for raising antibodies which can be used in diagnostic assays for
CC detection of Tango, and also for generating anti-idiotype antibodies for
CC prevention and protection.
SQ Sequence 3569 BP; 893 A; 821 C; 862 G; 993 T;

Query Match 36.6%; Score 432; DB 1; Length 3569;
Best Local Similarity 77.6%; Pred. No. 1.9e-82;
Matches 582; Conservative 0; Mismatches 145; Indels 23; Gaps 4;

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Qy      1 GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGA 60
          ||||  | ||||||  | |||||||||  ||||   |   ||||||||||||  |||||||||
Db     18 GCTGCGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTTGGCG 77

Qy     61 GTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGAC 120
           |||                     ||    | |      |      | |  ||  |||  |||||||
Db     78 CTTTC------------------GATCCACCCTCCTCCCTTCTCATGGGACTTTGGGGAC 119

Qy    121 AGAGCGCCCCGGCCGCCT-GATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGT 179
          | ||||  ||||  ||||||  ||  ||    ||||||  ||  | ||||||  |||||||  ||||
Db    120 AAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCAGGACAGCGT 179

Qy    180 CGGGAACCATACCATGGC-CCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCG 238
          ||||||||  |||||||  ||  |   | ||||||  |||  ||||||||||||  |||||||||
Db    180 CGGGAACCAGACCATGGCTCCTGGACTCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCG 239

Qy    239 CGGTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCC 298
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SUMMARIES

% **Apo-2DcR**

Result No.	Score	Query Match	Length	DB	ID	Description
1	1180	100.0	1180	24	US-08-878-168-2	Sequence 2, Appli
2	1180	100.0	1180	24	US-08-878-168-4	Sequence 4, Appli
3	1180	100.0	1180	24	US-08-878-168-2	Sequence 2, Appli
4	1180	100.0	1180	24	US-08-878-168-4	Sequence 4, Appli
5	1180	100.0	1180	37	US-09-096-500-2	Sequence 2, Appli
6	1180	100.0	1180	37	US-09-096-500-4	Sequence 4, Appli
7	1116.8	94.6	1121	1	PCT-US99-05243-7	Sequence 7, Appli
8	1116.8	94.6	1121	36	US-09-079-124-1	Sequence 1, Appli
9	1116.8	94.6	1121	42	US-09-266-105-7	Sequence 7, Appli
10	1104.4	93.6	1410	20	US-08-795-910-1	Sequence 1, Appli
11	1104.4	93.6	1410	25	US-08-901-469-1	Sequence 1, Appli
12	1103	93.5	1392	34	US-09-006-353A-1	Sequence 1, Appli
13	1103	93.5	1392	55	US-60-035-496-1	Sequence 1, Appli
14	1069.2	90.6	1365	27	US-08-924-634A-5	Sequence 5, Appli
15	1057	89.6	1347	1	PCT-US98-13491-1	Sequence 1, Appli
16	1057	89.6	1347	24	US-08-883-529-1	Sequence 1, Appli
17	1057	89.6	1347	40	US-09-229-980-1	Sequence 1, Appli